RAW SEQUENCE LISTING   DATE: 07/25/2002
PATENT APPLICATION: US/09/686,647   TIME: 14:30:35

Input Set : N:\Crf3\RULE60\09686647.raw
Output Set: N:\CRF3\07252002\I686647.raw

SEQUENCE LISTING

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 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: THE ROCKEFELLER UNIVERSITY
 7     (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
 8                             ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
10    (iii) NUMBER OF SEQUENCES: 38
12     (iv) CORRESPONDENCE ADDRESS:
13          (A) ADDRESSEE: Klauber & Jackson
14          (B) STREET: 411 Hackensack Avenue
15          (C) CITY: Hackensack
16          (D) STATE: New Jersey
17          (E) COUNTRY: USA
18          (F) ZIP: 07601
20      (v) COMPUTER READABLE FORM:
21          (A) MEDIUM TYPE: Floppy disk
22          (B) COMPUTER: IBM PC compatible
23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26     (vi) CURRENT APPLICATION DATA:
C--> 27     (A) APPLICATION NUMBER: US/09/686,647
C--> 28     (B) FILING DATE: 10-Oct-2000
38          (C) CLASSIFICATION:
31    (vii) PRIOR APPLICATION DATA:
33          (A) APPLICATION NUMBER: US/09/183,374
34          (B) FILING DATE:
36          (A) APPLICATION NUMBER: 08/347,563
37          (B) FILING DATE:
40   (viii) ATTORNEY/AGENT INFORMATION:
41          (A) NAME: Jackson Esq., David A.
42          (B) REGISTRATION NUMBER: 26,742
43          (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP
45     (ix) TELECOMMUNICATION INFORMATION:
46          (A) TELEPHONE: 201 487-5800
47          (B) TELEFAX: 201 343-1684
48          (C) TELEX: 133521
51 (2) INFORMATION FOR SEQ ID NO: 1:
53      (i) SEQUENCE CHARACTERISTICS:
54          (A) LENGTH: 2793 base pairs
55          (B) TYPE: nucleic acid
56          (C) STRANDEDNESS: double
57          (D) TOPOLOGY: linear
59     (ii) MOLECULE TYPE: DNA (genomic)
60          (A) DESCRIPTION: Murine ob cDNA
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ENTERED

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          RAW SEQUENCE LISTING              DATE: 07/25/2002
          PATENT APPLICATION: US/09/686,647   TIME: 14:30:35

          Input Set : N:\Crf3\RULE60\09686647.raw
          Output Set: N:\CRF3\07252002\I686647.raw

62    (iii) HYPOTHETICAL: NO
64     (iv) ANTI-SENSE: NO
66     (vi) ORIGINAL SOURCE:
67           (A) ORGANISM: Murine
68     (ix) FEATURE:
69           (A) NAME/KEY: CDS
70           (B) LOCATION: 57..560
73     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA          56
77 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG       104
78 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
79  1               5                   10                  15
81 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA       152
82 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
83              20                  25                  30
85 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG      200
86 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
87          35                  40                  45
89 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT       248
90 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
91      50                  55                  60
93 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA       296
94 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
95  65                  70                  75                  80
97 GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG       344
98 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
99                  85                  90                  95
101 ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC      392
102 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
103              100                 105                 110
105 TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA      440
106 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
107              115                 120                 125
109 GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG      488
110 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
111      130                 135                 140
113 GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG      536
114 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
115 145                 150                 155                 160
117 TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA       588
118 Leu Asp Val Ser Pro Glu Cys
119              165
121 ATCATGTAGA GGGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC   648
123 ACACATCCAT CATTCATTTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA   708
125 CAATGCTTGA CTCAAGTTAT CCACACAACT TCATGAGCAC AAGGAGGGGC CAGCCTGCAG   768
127 AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG   828
129 TCCCACCTGC TCCGGGTACA TGTTCCTCCG TGGGTACACG CTTCGCTGCG GCCCAGGAGA   888
131 GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA   948
133 GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT  1008
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Output Set: **N:\CRF3\07252002\I686647.raw**

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137 GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG   1128
139 CCCGAGGCAA ACCTAATTTT TGAGTGACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG   1188
141 TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTTTCT ATTGTGACTG   1248
143 ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA   1308
145 AGCAGATGAA TTTTGTCAAG TGTAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG   1368
147 TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT   1428
149 TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG   1488
151 ACAAAGGAGT TGACTCTTTC CGGAACATTT GGAGTGTACC AGGCACCCTT GGAGGGGCTA   1548
153 AAGCTACAGG CCTTTTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTTGA   1608
155 GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT   1668
157 CTCACAATGC GTTTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA   1728
159 TTGGTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT   1788
161 GGGAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT   1848
163 GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG   1908
165 CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AAACTGGGGG GCAGATCAGT   1968
167 GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT   2028
169 CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG   2088
171 TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCGCTG   2148
173 GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA   2208
175 GGGGAACCCT GCTTGCAGTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC   2268
177 CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA   2328
179 TCCAAAATGC TTGGGACTAG AAGAGTTTTG GATTTTAGAG TCTTTTCAGG CATAGGTATA   2388
181 TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC   2448
183 ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTTA   2508
185 AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA   2568
187 CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT   2628
189 AGCTTATACC TAAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC   2688
191 TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG   2748
193 GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC                    2793
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196 (2) INFORMATION FOR SEQ ID NO: 2:
197   (i) SEQUENCE CHARACTERISTICS:
198   (A) LENGTH: 167 amino acids
199   (B) TYPE: amino acid
200   (D) TOPOLOGY: linear
202   (ii) MOLECULE TYPE: protein
203   (A) DESCRIPTION: Murine ob polypeptide
205   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
207 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
208   1   5   10   15
210 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
211   20   25   30
213 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
214   35   40   45
216 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
217   50   55   60
219 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
220 65   70   75   80
222 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln

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223                  85                  90                  95
225 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
226             100                 105                 110
228 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
229         115                 120                 125
231 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
232     130                 135 ·               140
234 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
235 145                 150                 155                 160
237 Leu Asp Val Ser Pro Glu Cys
238                 165
241 (2) INFORMATION FOR SEQ ID NO: 3:
243        (i) SEQUENCE CHARACTERISTICS:
244            (A) LENGTH: 700 base pairs
245            (B) TYPE: nucleic acid
246            (C) STRANDEDNESS: double
247            (D) TOPOLOGY: linear
249      (ii) MOLECULE TYPE: cDNA
250            (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
252     (iii) HYPOTHETICAL: NO
254      (iv) ANTI-SENSE: NO
256      (vi) ORIGINAL SOURCE:
257            (A) ORGANISM: Human
259      (ix) FEATURE:
260            (A) NAME/KEY: CDS
261            (B) LOCATION: 46..546
264      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
266 NNNGNNGTTG CAAGGCCCAA GAAGCCCANN NTCCTGGGAA GGAAA ATG CAT TGG         54
267                                                     Met His Trp
268                                                      1
270 GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC    102
271 Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val
272     5                  10                  15
274 CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC    150
275 Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile
276 20                  25                  30                  35
278 AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC    198
279 Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val
280                 40                  45                  50
282 TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC    246
283 Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
284             55                  60                  65
286 CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA    294
287 Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln
288         70                  75                  80
290 CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC    342
291 Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn
292     85                  90                  95
294 GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG    390
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                    RAW SEQUENCE LISTING              DATE: 07/25/2002
                    PATENT APPLICATION:  US/09/686,647   TIME: 14:30:35

                    Input Set : N:\Crf3\RULE60\09686647.raw
                    Output Set: N:\CRF3\07252002\I686647.raw


295 Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys
296 100               105               110               115
298 AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG        438
299 Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu
300               120               125               130
302 GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG        486
303 Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu
304               135               140               145
306 AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC        534
307 Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu
308               150               155               160
310 AGC CCT GGG TGC TGAGGCCTT GAAGGTCACT CTTCCTGCAA GGACTNACGT             585
311 Ser Pro Gly Cys
312       165
314 TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC      645
316 CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG           700
319 (2) INFORMATION FOR SEQ ID NO: 4:
321       (i) SEQUENCE CHARACTERISTICS:
322             (A) LENGTH: 167 amino acids
323             (B) TYPE: amino acid
324             (D) TOPOLOGY: linear
326       (ii) MOLECULE TYPE: protein
327             (A) DESCRIPTION: Human ob polypeptide
329       (vi) ORIGINAL SOURCE:
331       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
333 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
334 1               5               10               15
336 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
337               20               25               30
339 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
340               35               40               45
342 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
343       50               55               60
345 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
346 65               70               75               80
348 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
349               85               90               95
351 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
352               100               105               110
355 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
356       115               120               125
359 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
360       130               135               140
362 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
363 145               150               155               160
366 Leu Asp Leu Ser Pro Gly Cys
367               165
370 (2) INFORMATION FOR SEQ ID NO: 5:
372       (i) SEQUENCE CHARACTERISTICS:
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VERIFICATION SUMMARY   DATE: 07/25/2002
PATENT APPLICATION: US/09/686,647   TIME: 14:30:36

Input Set : **N:\Crf3\RULE60\09686647.raw**
Output Set: **N:\CRF3\07252002\I686647.raw**

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L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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